

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/732,350DATE: 03/15/2001
TIME: 22:37:44

INPUT SET: S36514.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information

(i) APPLICANT: Svendsen, Allan
Xu, Feng

(ii) TITLE OF THE INVENTION: LACCASE MUTANTS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Novo Nordisk of North America, Inc.

(B) STREET: 405 Lexington Avenue

(C) CITY: New York

(D) STATE: NY

(E) COUNTRY: USA

(F) ZIP: 10174

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/732,350

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/032,315

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Rozek, Carol

(B) REGISTRATION NUMBER: 36,993

(C) REFERENCE/DOCKET NUMBER: 5200.200-US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-867-0123

(B) TELEFAX: 212-878-9655

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47
48 (2) INFORMATION FOR SEQ ID NO: 1:
49
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 539 amino acids
52 (B) TYPE: amino acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
55
56 (ii) MOLECULE TYPE: protein
57
58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
59
60 Met Phe Lys Asn Leu Leu Ser Phe Ala Leu Leu Ala Ile Ser Val Ala
61 1 5 10 15
62
63 Asn Ala Gln Ile Val Asn Ser Val Asp Thr Met Thr Leu Thr Asn Ala
64 20 25 30
65
66 Asn Val Ser Pro Asp Gly Phe Thr Arg Ala Gly Ile Leu Val Asn Gly
67 35 40 45
68
69 Val His Gly Pro Leu Ile Arg Gly Gly Lys Asn Asp Asn Phe Glu Leu
70 50 55 60
71
72 Asn Val Val Asn Asp Leu Asp Asn Pro Thr Met Leu Arg Pro Thr Ser
73 65 70 75 80
74
75 Ile His Trp His Gly Leu Phe Gln Arg Gly Thr Asn Trp Ala Asp Gly
76 85 90 95
77
78 Ala Asp Gly Val Asn Gln Cys Pro Ile Ser Pro Gly His Ala Phe Leu
79 100 105 110
80
81 Tyr Lys Phe Thr Pro Ala Gly His Ala Gly Thr Phe Trp Tyr His Ser
82 115 120 125
83
84 His Phe Gly Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Met Val Ile
85 130 135 140
86
87 Tyr Asp Asp Asn Asp Pro His Ala Ala Leu Tyr Asp Glu Asp Asp Glu
88 145 150 155 160
89 Asn Thr Ile Ile Thr Leu Ala Asp Trp Tyr His Ile Pro Ala Pro Ser
90 165 170 175
91
92 Ile Gln Gly Ala Ala Gln Pro Asp Ala Thr Leu Ile Asn Gly Lys Gly
93 180 185 190
94
95 Arg Tyr Val Gly Gly Pro Ala Ala Glu Leu Ser Ile Val Asn Val Glu
96 195 200 205
97
98 Gln Gly Lys Lys Tyr Arg Met Arg Leu Ile Ser Leu Ser Cys Asp Pro
99 210 215 220

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100	
101	Asn Trp Gln Phe Ser Ile Asp Gly His Glu Leu Thr Ile Ile Glu Val
102	225 230 235 240
103	
104	Asp Gly Gln Leu Thr Glu Pro His Thr Val Asp Arg Leu Gln Ile Phe
105	245 250 255
106	
107	Thr Gly Gln Arg Tyr Ser Phe Val Leu Asp Ala Asn Gln Pro Val Asp
108	260 265 270
109	
110	Asn Tyr Trp Ile Arg Ala Gln Pro Asn Lys Gly Arg Asn Gly Leu Ala
111	275 280 285
112	
113	Gly Thr Phe Ala Asn Gly Val Asn Ser Ala Ile Leu Arg Tyr Ala Gly
114	290 295 300
115	
116	Ala Ala Asn Ala Asp Pro Thr Thr Ser Ala Asn Pro Asn Pro Ala Gln
117	305 310 315 320
118	
119	Leu Asn Glu Ala Asp Leu His Ala Leu Ile Asp Pro Ala Ala Pro Gly
120	325 330 335
121	
122	Ile Pro Thr Pro Gly Ala Ala Asp Val Asn Leu Arg Phe Gln Leu Gly
123	340 345 350
124	
125	Phe Ser Gly Gly Arg Phe Thr Ile Asn Gly Thr Ala Tyr Glu Ser Pro
126	355 360 365
127	
128	Ser Val Pro Thr Leu Leu Gln Ile Met Ser Gly Ala Gln Ser Ala Asn
129	370 375 380
130	
131	Asp Leu Leu Pro Ala Gly Ser Val Tyr Glu Leu Pro Arg Asn Gln Val
132	385 390 395 400
133	
134	Val Glu Leu Val Val Pro Ala Gly Val Leu Gly Gly Pro His Pro Phe
135	405 410 415
136	
137	His Leu His Gly His Ala Phe Ser Val Val Arg Ser Ala Gly Ser Ser
138	420 425 430
139	
140	Thr Tyr Asn Phe Val Asn Pro Val Lys Arg Asp Val Val Ser Leu Gly
141	435 440 445
142	
143	Val Thr Gly Asp Glu Val Thr Ile Arg Phe Val Thr Asp Asn Pro Gly
144	450 455 460
145	
146	Pro Trp Phe Phe His Cys His Ile Glu Phe His Leu Met Asn Gly Leu
147	465 470 475 480
148	
149	Ala Ile Val Phe Ala Glu Asp Met Ala Asn Thr Val Asp Ala Asn Asn
150	485 490 495
151	
152	Pro Pro Val Glu Trp Ala Gln Leu Cys Glu Ile Tyr Asp Asp Leu Pro

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153          500          505          510
154
155
156      Pro Glu Ala Thr Ser Ile Gln Thr Val Val Arg Arg Ala Glu Pro Thr
157          515          520          525
158
159      Gly Phe Ser Ala Lys Phe Arg Arg Glu Gly Leu
160          530          535
161
162
163 (2) INFORMATION FOR SEQ ID NO: 2:
164
165     (i) SEQUENCE CHARACTERISTICS:
166         (A) LENGTH: 499 amino acids
167         (B) TYPE: amino acid
168         (C) STRANDEDNESS: single
169         (D) TOPOLOGY: linear
170
171     (ii) MOLECULE TYPE: protein
172
173     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
174
175      Gly Ile Gly Pro Val Ala Asp Leu Thr Ile Thr Asn Ala Ala Val Ser
176      1             5             10             15
177
178      Pro Asp Gly Phe Ser Arg Gln Ala Val Val Val Asn Gly Gly Thr Pro
179             20             25             30
180
181      Gly Pro Leu Ile Thr Gly Asn Met Gly Asp Arg Phe Gln Leu Asn Val
182             35             40             45
183
184      Ile Asp Asn Leu Thr Asn His Thr Met Leu Lys Ser Thr Ser Ile His
185             50             55             60
186
187      Trp His Gly Phe Phe Gln Lys Gly Thr Asn Trp Ala Asp Gly Pro Ala
188      65             70             75             80
189
190      Phe Ile Asn Gln Cys Pro Ile Ser Ser Gly His Ser Phe Leu Tyr Asp
191             85             90             95
192
193      Phe Gln Val Pro Asp Gln Ala Gly Thr Phe Trp Tyr His Ser His Leu
194             100            105            110
195
196      Ser Thr Gln Tyr Cys Asp Gly Leu Arg Gly Pro Phe Val Val Tyr Asp
197             115            120            125
198
199      Pro Asn Asp Pro Ala Ala Asp Leu Tyr Asp Val Asp Asn Asp Asp Thr
200             130            135            140
201
202      Val Ile Thr Leu Val Asp Trp Tyr His Val Ala Ala Lys Leu Gly Pro
203      145            150            155            160
204
205      Ala Phe Pro Leu Gly Ala Asp Ala Thr Leu Ile Asn Gly Lys Gly Arg

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206		165		170		175
207						
208	Ser	Pro	Ser	Thr	Thr	Thr
209				180		185
210						190
211	Gly	Lys	Arg	Tyr	Arg	Phe
212			195			200
213						205
214	Tyr	Thr	Phe	Ser	Ile	Asp
215		210			215	
216						220
217	Ser	Ile	Asn	Thr	Ala	Pro
218	225				230	
219						235
220	Ala	Gln	Arg	Tyr	Ser	Phe
221				245		250
222						255
223	Tyr	Trp	Ile	Arg	Ala	Asn
224			260			265
225						270
226	Gly	Ile	Asn	Ser	Ala	Ile
227		275			280	
228						285
229	Pro	Thr	Thr	Thr	Gln	Thr
230		290			295	
231						300
232	Leu	His	Pro	Leu	Val	Thr
233	305				310	
234						315
235	Gly	Val	Asp	Leu	Ala	Ile
236				325		330
237						335
238	Phe	Phe	Ile	Asn	Gly	Ala
239				340		345
240						350
241	Leu	Gln	Ile	Ile	Ser	Gly
242		355				360
243						365
244	Gly	Ser	Val	Tyr	Ser	Leu
245		370			375	
246						380
247	Pro	Ala	Thr	Ala	Ala	Ala
248	385				390	
249						395
250	Gly	His	Ala	Phe	Ala	Val
251				405		410
252						415
253	Tyr	Asp	Asn	Pro	Ile	Phe
254			420			425
255						430
256	Ala	Gly	Asp	Asn	Val	Thr
257		435			440	
258						445

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text